

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Celeste, Anthony J.  
Wozney, John  
Rosen, Vicki A.  
Wolfman, Neil  
Melton, Douglas A.  
Thomsen, Gerald H.

(ii) TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

(iii) NUMBER OF SEQUENCES: 24

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: GENETICS INSTITUTE, INC.  
(B) STREET: 87 CambridgePark Drive  
(C) CITY: Cambridge  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US  
(B) FILING DATE:  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lazar, Steven R.  
(B) REGISTRATION NUMBER: 32,618  
(C) REFERENCE/DOCKET NUMBER: 5202-CIP

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617 876-1170  
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: v1-1

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 571..882

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..882

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCG CGT AAT ACG ACT CAC TAT AGG GCG AAT TGG GTA CGG GGC CCA GGC	48
Ala Arg Asn Thr Thr His Tyr Arg Ala Asn Trp Val Arg Gly Pro Gly	
-190 -185 -180 -175	
AGC TGG ACT TCT CCG CCG TTG CTG CTG CTG TCC ACG TGC CCG GGC GCC	96
Ser Trp Thr Ser Pro Pro Leu Leu Leu Ser Thr Cys Pro Gly Ala	
-170 -165 -160	
GCC CGA GCG CCA CGC CTG CTG TAC TCG CGG GCA GCT GAG CCC CTA GTC	144
Ala Arg Ala Pro Arg Leu Leu Tyr Ser Arg Ala Ala Glu Pro Leu Val	
-155 -150 -145	
GGT CAG CGC TGG GAG GCG TTC GAC GTG GCG GAC GCC ATG AGG CGC CAC	192
Gly Gln Arg Trp Glu Ala Phe Asp Val Ala Asp Ala Met Arg Arg His	
-140 -135 -130	
CGT CGT GAA CCG CGC CCC CCC CGC GCG TTC TGC CTC TTG CTG CGC GCA	240
Arg Arg Glu Pro Arg Pro Pro Arg Ala Phe Cys Leu Leu Leu Arg Ala	
-125 -120 -115	
GTG GCA GGC CCG GTG CCG AGC CCG TTG GCA CTG CGG CGA CTG GGC TTC	288
Val Ala Gly Pro Val Pro Ser Pro Leu Ala Leu Arg Arg Leu Gly Phe	
-110 -105 -100 -95	
GGC TGG CCG GGC GGA GGG GGC TCT GCG GCA GAG GAG CGC GCG GTG CTA	336
Gly Trp Pro Gly Gly Gly Ser Ala Ala Glu Glu Arg Ala Val Leu	
-90 -85 -80	
GTC GTC TCC TCC CGC ACG CAG AGG AAA GAG AGC TTA TTC CGG GAG ATC	384
Val Val Ser Ser Arg Thr Gln Arg Lys Glu Ser Leu Phe Arg Glu Ile	
-75 -70 -65	
CGC GCC CAG GCC CGC GCG CTC GGG GCC GCT CTG GCC TCA GAG CCG CTG	432
Arg Ala Gln Ala Arg Ala Leu Gly Ala Ala Leu Ala Ser Glu Pro Leu	
-60 -55 -50	
CCC GAC CCA GGA ACC GGC ACC GCG TCG CCA AGG GCA GTC ATT GGC GGC	480
Pro Asp Pro Gly Thr Gly Thr Ala Ser Pro Arg Ala Val Ile Gly Gly	
-45 -40 -35	
CGC AGA CGG AGG AGG ACG GCG TTG GCC GGG ACG CGG ACA GCG CAG GGC	528
Arg Arg Arg Arg Arg Thr Ala Leu Ala Gly Thr Arg Thr Ala Gln Gly	
-30 -25 -20 -15	
AGC GGC GGG GGC GCG GGC CGG GGC CAC GGG CGC AGG GGC CGG AGC CGC	576
Ser Gly Gly Gly Ala Gly Arg Gly His Gly Arg Arg Gly Arg Ser Arg	
-10 -5 1	
TGC AGC CGC AAG CCG TTG CAC GTG GAC TTC AAG GAG CTC GGC TGG GAC	624
Cys Ser Arg Lys Pro Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp	
5 10 15	

GAC TGG ATC ATC GCG CCG CTG GAC TAC GAG GCG TAC CAC TGC GAG GGC	672
Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly	
20 25 30	
CTT TGC GAC TTC CCT TTG CGT TCG CAC CTC GAG CCC ACC AAC CAT GCC	720
Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala	
35 40 45 50	
ATC ATT CAG ACG CTG CTC AAC TCC ATG GCA CCA GAC GCG GCG CCG GCC	768
Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala	
55 60 65	
TCC TGC TGT GTG CCA GCG CGC CTC AGC CCC ATC AGC ATC CTC TAC ATC	816
Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile	
70 75 80	
GAC GCC GCC AAC AAC GTT GTC TAC AAG CAA TAC GAG GAC ATG GTG GTG	864
Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val	
85 90 95	
GAG GCC TGC GGC TGC AGG TAGCGCGCGG GCCGGGGAGG GGGCAGCCAC	912
Glu Ala Cys Gly Cys Arg	
100	
GCGGCCGAGG ATCC	926

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Arg Asn Thr Thr His Tyr Arg Ala Asn Trp Val Arg Gly Pro Gly	
-190 -185 -180 -175	
Ser Trp Thr Ser Pro Pro Leu Leu Leu Ser Thr Cys Pro Gly Ala	
-170 -165 -160	
Ala Arg Ala Pro Arg Leu Leu Tyr Ser Arg Ala Ala Glu Pro Leu Val	
-155 -150 -145	
Gly Gln Arg Trp Glu Ala Phe Asp Val Ala Asp Ala Met Arg Arg His	
-140 -135 -130	
Arg Arg Glu Pro Arg Pro Pro Arg Ala Phe Cys Leu Leu Arg Ala	
-125 -120 -115	
Val Ala Gly Pro Val Pro Ser Pro Leu Ala Leu Arg Arg Leu Gly Phe	
-110 -105 -100 -95	
Gly Trp Pro Gly Gly Gly Ser Ala Ala Glu Glu Arg Ala Val Leu	
-90 -85 -80	
Val Val Ser Ser Arg Thr Gln Arg Lys Glu Ser Leu Phe Arg Glu Ile	
-75 -70 -65	

Arg Ala Gln Ala Arg Ala Leu Gly Ala Ala Leu Ala Ser Glu Pro Leu  
           -60                          -55                          -50  
  
 Pro Asp Pro Gly Thr Gly Thr Ala Ser Pro Arg Ala Val Ile Gly (Gly  
           -45                          -40                          -35  
  
 Arg Arg Arg Arg Arg Thr Ala Leu Ala Gly Thr Arg Thr Ala Gln Gly  
   -30                          -25                          -20                          -15  
  
 Ser Gly Gly Gly Ala Gly Arg Gly His Gly Arg Arg Gly Arg Ser Arg  
                           -10                          -5                          1  
  
 Cys Ser Arg Lys Pro Leu His Val Asp Phe Lys Glu Leu Gly Trp Asp  
           5                          10                          15  
  
 Asp Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly  
   20                          25                          30  
  
 Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala  
   35                          40                          45                          50  
  
 Ile Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala  
                           55                          60                          65  
  
 Ser Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile  
           70                          75                          80  
  
 Asp Ala Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val Val  
           85                          90                          95  
  
 Glu Ala Cys Gly Cys Arg  
   100

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1207 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: MP52
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 845..1204

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACCGGGCGGC CCTGAACCCA AGCCAGGACA CCCTCCCCAA ACAAGGCAGG CTACAGCCCCG 60  
 GACTGTGACC CCAAAGGAC AGCTTCCCGG AGGCAAGGCA CCCCAAAAG CAGGATCTGT 120

CCCCAGCTCC TTCCTGCTGA AGAAGGCCAG GGAGCCCGGG CCCCCACGAG AGCCCAAGGA	180
GCCGTTTCGC CCACCCCCCA TCACACCCCA CGAGTACATG CTCTCGCTGT ACAGGACGCT	240
GTCCGATGCT GACAGAAAGG GAGGCAACAG CAGCGTGAAG TTGGAGGCTG GCCTGGCCAA	300
CACCATCACC AGCTTTATTG ACAAAGGGCA AGATGACCGA GGTCCCGTGG TCAGGAAGCA	360
GAGGTACGTG TTTGACATTA GTGCCCTGGA GAAGGATGGG CTGCTGGGGG CCGAGCTCCG	420
GATCTTGCGG AAGAAGCCCT CGGACACGGC CAAGCCAGCG GCCCCCGGAG GCGGGCGGGC	480
TGCCCAGCTG AAGCTGTCCA GCTGCCCCAG CGGCCGGCAG CCGGCCTCCT TGCTGGATGT	540
GCGCTCCGTG CCAGGCCTGG ACGGATCTGG CTGGGAGGTG TTCGACATCT GGAAGCTCTT	600
CCGAAACTTT AAGAACTCGG CCCAGCTGTG CCTGGAGCTG GAGGCCTGGG AACGGGGCAG	660
GGCCGTGGAC CTCCGTGGCC TGGGCTTCGA CCGCGCCGCC CGGCAGGTCC ACGAGAAGGC	720
CCTGTTCTTG GTGTTTGGCC GCACCAAGAA ACGGGACCTG TTCTTTAATG AGATTAAGGC	780
CCGCTCTGGC CAGGACGATA AGACCGTGTA TGAGTACCTG TTCAGCCAGC GGCAGAAACG	840
GCGG GCC CCA CTG GCC ACT CGC CAG GGC AAG CGA CCC AGC AAG AAC CTT	889
Ala Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu	
1 5 10 15	
AAG GCT CGC TGC AGT CGG AAG GCA CTG CAT GTC AAC TTC AAG GAC ATG	937
Lys Ala Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met	
20 25 30	
GGC TGG GAC GAC TGG ATC ATC GCA CCC CTT GAG TAC GAG GCT TTC CAC	985
Gly Trp Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His	
35 40 45	
TGC GAG GGG CTG TGC GAG TTC CCA TTG CGC TCC CAC CTG GAG CCC ACG	1033
Cys Glu Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr	
50 55 60	
AAT CAT GCA GTC ATC CAG ACC CTG ATG AAC TCC ATG GAC CCC GAG TCC	1081
Asn His Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser	
65 70 75	
ACA CCA CCC ACC TGC TGT GTG CCC ACG CGG CTG AGT CCC ATC AGC ATC	1129
Thr Pro Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile	
80 85 90 95	
CTC TTC ATT GAC TCT GCC AAC AAC GTG GTG TAT AAG CAG TAT GAG GAC	1177
Leu Phe Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp	
100 105 110	
ATG GTC GTG GAG TCG TGT GGC TGC AGG TAG	1207
Met Val Val Glu Ser Cys Gly Cys Arg	
115 120	

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids  
 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Ala Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys
 1             5             10             15
Ala Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly
          20             25             30
Trp Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys
          35             40             45
Glu Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn
          50             55             60
His Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr
          65             70             75             80
Pro Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu
          85             90             95
Phe Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met
          100            105            110
Val Val Glu Ser Cys Gly Cys Arg
          115            120

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens

(vii) IMMEDIATE SOURCE:

- (B) CLONE: V1-1 fragment

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

GGATCCTGGA AGGATTGGAT CATTGCG CCG CTG GAC TAC GAG GCG TAC CAC      51
          Pro Leu Asp Tyr Glu Ala Tyr His
          1             5
TGC GAG GGC CTT TGC GAC TTC CCT TTG CGT TCG CAC CTC GAG CCC ACC      99
Cys Glu Gly Leu Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr

```

10 15 20 128

AAC CACGCTATAG TCCAAACCTT TCTAGA  
 Asn  
 25

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly Leu Cys Asp Phe Pro  
 1 5 10 15  
 Leu Arg Ser His Leu Glu Pro Thr Asn  
 20 25

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo Sapiens

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: VL-1

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 28..102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCTGGG ATGACTGGAT TATGGCG CCG CTG GAC TAC GAG GCG TAC CAC 51  
 Pro Leu Asp Tyr Glu Ala Tyr His  
 1 5  
 TGC GAG GGT GTA TGC GAC TTC CCG CTG CGC TCG CAC CTG GAG CCC ACC 99  
 Cys Glu Gly Val Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr  
 10 15 20  
 AAC CACGCCATGC TACAAACGCT TCTAGA 128  
 Asn  
 25

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly Val Cys Asp Phe Pro  
 1 5 10 15  
 Leu Arg Ser His Leu Glu Pro Thr Asn  
 20 25

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: pALV1-781

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTAACTACCC AACTCAAAAA AAAAAAAAAA AAAAACCCCC TCTAACCCCC ATTGACGAAA	60
GGGCCTCGTG ATACGCCTAT TTTTATAGGT TAATGTCATG ATAATAATGG TTTCTTAGAC	120
GTCAGGTGGC ACTTTTCGGG GAAATGTGCG CGGAACCCCT ATTTGTTTAT TTTTCTAAAT	180
ACATTCAAAT ATGTATCCGC TCATGAGACA ATAACCCTGA TAAATGCTTC AATAATATTG	240
AAAAAGGAAG AGTATGAGTA TTCAACATTT CCGTGTGCGC CTTATTCCCT TTTTTCGGGC	300
ATTTTGCCTT CCTGTTTTTG CTCACCCAGA AACGCTGGTG AAAGTAAAAG ATGCTGAAGA	360
TCAGTTGGGT GCACGAGTGG GTTACATCGA ACTGGATCTC AACAGCGGTA AGATCCTTGA	420
GAGTTTTTCGC CCCGAAGAAC GTTTTCCAAT GATGAGCACT TTTAAAGTTC TGCTATGTGG	480
CGCGGTATTA TCCCGTATTG ACGCCGGGCA AGAGCAACTC GGTCCGCCGA TACACTATTG	540
TCAGAATGAC TTGGTTGAGT ACTCACCAGT CACAGAAAAG CATCTTACGG ATGGCATGAC	600
AGTAAGAGAA TTATGCAGTG CTGCCATAAC CATGAGTGAT AACACTGCGG CCAACTTACT	660
TCTGACAACG ATCGGAGGAC CGAAGGAGCT AACCCTTTT TTGCACAACA TGGGGGATCA	720
TGTAACFCGC CTTGATCGTT GGAACCGGA GCTGAATGAA GCCATACCAA ACGACGAGCG	780
TGACACCACG ATGCCTGTAG CAATGGCAAC AACGTTGCGC AACTATTAA CTGGCGAACT	840
ACTTACTCTA GCTTCCCGGC AACAATTAAT AGACTGGATG GAGGCGGATA AAGTTGCAGG	900



ACCACTTCTG	CGCTCGGCCC	TTCCGGCTGG	CTGGTTTATT	GCTGATAAAT	CTGGAGCCGG	960
TGAGCGTGGG	TCTCGCGGTA	TCATTGCAGC	ACTGGGGCCA	GATGGTAAGC	CCTCCCGTAT	1020
CGTAGTTATC	TACACGACGG	GGAGTCAGGC	AACTATGGAT	GAACGAAATA	GACAGATCGC	1080
TGAGATAGGT	GCCTCACTGA	TTAAGCATTG	GTAAGTGTCA	GACCAAGTTT	ACTCATATAT	1140
ACTTTAGATT	GATTTAAAC	TTCATTTTTA	ATTTAAAAGG	ATCTAGGTGA	AGATCCTTTT	1200
TGATAATCTC	ATGACCAAAA	TCCCTTAACG	TGAGTTTTTCG	TTCCACTGAG	CGTCAGACCC	1260
CGTAGAAAAG	ATCAAAGGAT	CTTCTTGAGA	TCCTTTTTTTT	CTGCGCGTAA	TCTGCTGCTT	1320
GCAAACAAAA	AAACCACCGC	TACCAGCGGT	GGTTTGTTTG	CCGGATCAAG	AGCTACCAAC	1380
TCTTTTTCCG	AAGGTAAGT	GCTTCAGCAG	AGCGCAGATA	CCAAATACTG	TCCTTCTAGT	1440
GTAGCCGTAG	TTAGGCCACC	ACTTCAAGAA	CTCTGTAGCA	CCGCCTACAT	ACCTCGCTCT	1500
GCTAATCCTG	TTACCAGTGG	CTGCTGCCAG	TGGCGATAAG	TCGTGTCTTA	CCGGGTGGA	1560
CTCAAGACGA	TAGTTACCGG	ATAAGGCGCA	GCGGTCGGGC	TGAACGGGGG	GTTGCTGCAC	1620
ACAGCCCAGC	TTGGAGCGAA	CGACCTACAC	CGAACTGAGA	TACCTACAGC	GTGAGCATTG	1680
AGAAAGCGCC	ACGCTTCCCG	AAGGGAGAAA	GGCGGACAGG	TATCCGGTAA	GCGGCAGGGT	1740
CGGAACAGGA	GAGCGCACGA	GGGAGCTTCC	AGGGGGAAAC	GCCTGGTATC	TTTATAGTCC	1800
TGTCGGGTTT	CGCCACCTCT	GACTTGAGCG	TCGATTTTTG	TGATGCTCGT	CAGGGGGGCG	1860
GAGCCTATGG	AAAAACGCCA	GCAACGCGGC	CTTTTTACGG	TTCCTGGCCT	TTTGCTGGCC	1920
TTTTGCTCAC	ATGTTCTTTC	CTGCGTTATC	CCCTGATTCT	GTGGATAACC	GTATTACCGC	1980
CTTTGAGTGA	GCTGATACCG	CTCGCCGCAG	CCGAACGACC	GAGCGCAGCG	AGTCAGTGAG	2040
CGAGGAAGCG	GAAGAGCGCC	CAATACGCAA	ACCGCCTCTC	CCCGCGCGTT	GGCCGATTCA	2100
TTAATGCAGA	ATTGATCTCT	CACCTACCAA	ACAATGCCCC	CCTGCAAAAA	ATAAATTCAT	2160
ATAAAAAACA	TACAGATAAC	CATCTGCGGT	GATAAATTAT	CTCTGGCGGT	GTTGACATAA	2220
ATACCACTGG	CGGTGATACT	GAGCACATCA	GCAGGACGCA	CTGACCACCA	TGAAGGTGAC	2280
GCTCTTAAAA	ATTAAGCCCT	GAAGAAGGGC	AGCATTCAAA	GCAGAAGGCT	TTGGGGTGTG	2340
TGATACGAAA	CGAAGCATTG	GCCGTAAGTG	CGATTCCGGA	TTAGCTGCCA	ATGTGCCAAT	2400
CGCGGGGGGT	TTTCGTTTCA	GACTACAAC	GCCACACACC	ACCAAAGCTA	ACTGACAGGA	2460
GAATCCAGAT	GGATGCACAA	ACACGCCGCC	GCGAACGTCG	CGCAGAGAAA	CAGGCTCAAT	2520
GGAAAGCAGC	AAATCCCCTG	TTGGTTGGGG	TAAGCGCAAA	ACCAGTTCCG	AAAGATTTTT	2580
TTAACTATAA	ACGCTGATGG	AAGCGTTTAT	GCGGAAGAGG	TAAAGCCCTT	CCCGAGTAAC	2640
AAAAAAACAA	CAGCATAAAT	AACCCCGCTC	TTACACATTC	CAGCCCTGAA	AAAGGGCATC	2700
AAATTAAACC	ACACCTATGG	TGTATGCATT	TATTTGCATA	CATTCAATCA	ATTGTTATCT	2760

AAGGAAATAC	TTACATATGT	CTCGTTGTTC	TCGTAACCA	CTGCATGTAG	ATTTTAAAGA	2820
GCTCGGCTGG	GACGACTGGA	TCATCGCGCC	GCTGGACTAC	GAGGCGTACC	ACTGCGAGGG	2880
CCTTTGCGAC	TTCCCTTTGC	GTTCGCACCT	CGAGCCCACC	AACCATGCCA	TCATTGAGAC	2940
GCTGCTCAAC	TCCATGGCAC	CAGACGCGGC	GCCGGCCTCC	TGCTGTGTGC	CAGCGCGCCT	3000
CAGCCCCATC	AGCATCCTCT	ACATCGACGC	CGCCAACAAC	GTTGTCTACA	AGCAATACGA	3060
GGACATGGTG	GTGGAGGCCT	GCGGCTGCAG	GTAGTCTAGA	GTCGACCTGC	AGTAATCGTA	3120
CAGGGTAGTA	CAAATAAAAA	AGGCACGTCA	GATGACGTGC	CTTTTTTCTT	GTGAGCAGTA	3180
AGCTTGGCAC	TGGCCGTCGT	TTTACAACGT	CGTGACTGGG	AAAACCCCTG	CGTTACCCAA	3240
CTTAATCGCC	TTGCAGCACA	TCCCCCTTTC	GCCAGCTGGC	GTAATAGCGA	AGAGGCCCGC	3300
ACCGATCGCC	CTTCCCAACA	GTTGCGCAGC	CTGAATGGCG	AATGGCGCCT	GATGCGGTAT	3360
TTTCTCCTTA	CGCATCTGTG	CGGTATTTCA	CACCGCATAT	ATGGTGCAC	CTCAGTACAA	3420
TCTGCTCTGA	TGCCGCATAG	TTAAGCCAGC	CCCGACACCC	GCCAACACCC	GCTGACGCGC	3480
CCTGACGGGC	TTGTCTGCTC	CCGGCATCCG	CTTACAGACA	AGCTGTGACC	GTCTCCGGGA	3540
GCTGCATGTG	TCAGAGGTTT	TCACCGTCAT	CACCGAAACG	CGCGA		3585

(2) INFORMATION FOR SEQ ID NO:10:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 272 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: mouse

(vii) IMMEDIATE SOURCE:
      (B) CLONE: mV1

(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 28..243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
```

[illegible]

GCG CCC GAC GCT GCG CCA GCC TCC TGC TGC GTG CCC GCA AGG CTC AGT 195  
 Ala Pro Asp Ala Ala Pro Ala Ser Cys Cys Val Pro Ala Arg Leu Ser  
                     45                    50                    55

CCC ATC AGC ATT CTC TAC ATC GAT GCC GCC AAC AAC GTG GTC TAC AAG 243  
 Pro Ile Ser Ile Leu Tyr Ile Asp Ala Ala Asn Asn Val Val Tyr Lys  
                     60                    65                    70

CAATACGAGG ACATGGTGGT GGGGAATTC 272

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Trp Ile Ile Ala Pro Leu Asp Tyr Glu Ala Tyr His Cys Glu Gly Val  
   1                    5                    10                    15

Cys Asp Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Ile  
                     20                    25                    30

Ile Gln Thr Leu Leu Asn Ser Met Ala Pro Asp Ala Ala Pro Ala Ser  
                     35                    40                    45

Cys Cys Val Pro Ala Arg Leu Ser Pro Ile Ser Ile Leu Tyr Ile Asp  
                     50                    55                    60

Ala Ala Asn Asn Val Val Tyr Lys  
   65                    70

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: mouse

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: mv2

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 28..243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGATCCAAGG AGCTCGGCTG GGACGAC TGG ATT ATC GCG CCC CTA GAG TAC 51  
                     Trp Ile Ile Ala Pro Leu Glu Tyr  
                     1                    5

|            |            |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|------------|------------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GAG        | GCC        | TAT       | CAC | TGC | GAG | GGC | GTG | TGC | GAC | TTT | CCG | CTG | CGC | TCG | CAC | 99  |
| Glu        | Ala        | Tyr       | His | Cys | Glu | Gly | Val | Cys | Asp | Phe | Pro | Leu | Arg | Ser | His |     |
| 10         |            |           |     |     | 15  |     |     |     |     | 20  |     |     |     |     |     |     |
|            |            |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CTT        | GAG        | CCC       | ACT | AAC | CAT | GCC | ATC | ATT | CAG | ACG | CTG | ATG | AAC | TCC | ATG | 147 |
| Leu        | Glu        | Pro       | Thr | Asn | His | Ala | Ile | Ile | Gln | Thr | Leu | Met | Asn | Ser | Met |     |
| 25         |            |           |     | 30  |     |     |     |     | 35  |     |     |     |     |     | 40  |     |
|            |            |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GAC        | CCG        | GGC       | TCC | ACC | CCG | CCT | AGC | TGC | TGC | GTT | CCC | ACC | AAA | CTG | ACT | 195 |
| Asp        | Pro        | Gly       | Ser | Thr | Pro | Pro | Ser | Cys | Cys | Val | Pro | Thr | Lys | Leu | Thr |     |
|            |            |           |     | 45  |     |     |     | 50  |     |     |     |     |     | 55  |     |     |
|            |            |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CCC        | ATT        | AGC       | ATC | CTG | TAC | ATC | GAC | GCG | GGC | AAT | AAT | GTA | GTC | TAC | AAG | 243 |
| Pro        | Ile        | Ser       | Ile | Leu | Tyr | Ile | Asp | Ala | Gly | Asn | Asn | Val | Val | Tyr | Lys |     |
|            |            |           | 60  |     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |
|            |            |           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CAATACGAGG | ACATGGTGGT | GGGGAATTC |     |     |     |     |     |     |     |     |     |     |     |     |     | 272 |

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ile | Ile | Ala | Pro | Leu | Glu | Tyr | Glu | Ala | Tyr | His | Cys | Glu | Gly | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Cys | Asp | Phe | Pro | Leu | Arg | Ser | His | Leu | Glu | Pro | Thr | Asn | His | Ala | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ile | Gln | Thr | Leu | Met | Asn | Ser | Met | Asp | Pro | Gly | Ser | Thr | Pro | Pro | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Cys | Cys | Val | Pro | Thr | Lys | Leu | Thr | Pro | Ile | Ser | Ile | Leu | Tyr | Ile | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Ala | Gly | Asn | Asn | Val | Val | Tyr | Lys |     |     |     |     |     |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: mouse

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: mV9

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 28..243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GGATCCAAGG AGCTCGGCTG GGACGAC TGG ATC ATC GCA CCT CTT GAG TAT      51
                    Trp Ile Ile Ala Pro Leu Glu Tyr
                      1                     5

GAG GCC TTC CAC TGC GAA GGA CTG TGT GAG TTC CCC TTG CGC TCC CAC      99
Glu Ala Phe His Cys Glu Gly Leu Cys Glu Phe Pro Leu Arg Ser His
    10                15                20

TTG GAG CCC ACA AAC CAC GCA GTC ATT CAG ACC CTA ATG AAC TCT ATG      147
Leu Glu Pro Thr Asn His Ala Val Ile Gln Thr Leu Met Asn Ser Met
    25                30                35                40

GAC CCT GAA TCC ACA CCA CCC ACT TGT TGT GTG CCT ACA CGG CTG AGT      195
Asp Pro Glu Ser Thr Pro Pro Thr Cys Cys Val Pro Thr Arg Leu Ser
                45                50                55

CCT ATT AGC ATC CTC TTC ATC GAC TCT GCC AAC AAC GTG GTG TAT AAA      243
Pro Ile Ser Ile Leu Phe Ile Asp Ser Ala Asn Asn Val Val Tyr Lys
    60                65                70

CAATACGAGG ACATGGTGGT GGGGAATTC      272

```

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu Gly Leu
  1                     5                     10                    15

Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His Ala Val
    20                25                30

Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro Pro Thr
    35                40                45

Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe Ile Asp
    50                55                60

Ser Ala Asn Asn Val Val Tyr Lys
    65                70

```

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: BMP/TGF-beta consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Trp Xaa Asp Trp Ile Xaa Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: oligonucleotide #1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGATCCTGG VANGAYTGGA THRTNGC

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: BMP/TGF-beta consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Ala Ile Xaa Gln Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: oligonucleotide #2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TTTCTAGAAR NGTYTGNACD ATNGCRTG

28

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: oligonucleotide #3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCACTGCGAG GGCCTTTGCG ACTTCCCTTT GCGTTCGCAC

40

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: oligonucleotide #4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TGCGGATCCA GCCGCTGCAG CCGCAAGCC

29

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

(B) CLONE: oligonucleotide #5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACTCTAGAC TACCTGCAGC CGCAGGCCT

29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: oligonucleotide #6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGGATCCAA GGAGCTCGGC TGGGACGA

28

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: oligonucleotide #7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGAATTCCTCC ACCACCATGT CCTCGTAT

28